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GenCore version 5.1.6

OM protein - protein search, using sw model
Run on: March 7, 2005, 07:04:17 ; Search time 4.6765 Seconds
(without alignments)
1193.323 Million cell updates/sec

Title: US-09-939-537-35
Perfect score: 288
Sequence: 1 PRASALPAPPTGALPDQTVISPLGLGGLGVACVLARTR 58
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*

1: pirl:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	284	98.6	240	A39016	T-cell surface glycoprotein CD7 precursor - human
2	80	27.8	421	T30709	Nt Alternate name: T-cell leukemia antigen
3	77	26.7	375	T0134	CSpecies: Homo sapiens (man)
4	76.5	26.6	710	D98728	CDate: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 09-Jul-2004
5	75	26.0	539	T28770	Accession: A39016; S03520
6	75	26.0	891	G84693	R.Schamburg, L.B.; Fleenor, D.B.; Kurtzberg, J.; Haynes, B.F.; Kaufman, R.E.
7	74	25.7	464	S22697	Proc. Natl. Acad. Sci., U.S.A., 88, 603-607, 1991
8	73	25.3	215	S63966	A:Title: Isolation and characterization of the genomic human CD7 gene: structural similar
9	73	25.3	418	G03953	A:Reference number: A39016; MUID:91110576; PMID:1703303
10	73	25.3	482	T36045	A:Status: Preliminary
11	73	25.3	614	E86194	A:Molecule type: DNA
12	71	24.7	662	T06600	A:Cross-references: UNIPROT:P09564; GB:M37271; NID:9180163; PID:AA51953.1; PID:g180164
13	70.5	24.5	559	C75286	R.Aruffo, A.; Seed, B. Seed, R.; Aruffo, J., 3313-3316, 1987
14	70.5	24.5	660	1 Q8B33	A:Title: Molecular cloning of two CD7 (T-cell leukemia antigen) cDNAs by a COS cell expr
15	69.5	24.1	1249	T41150	A:Reference number: S03520; MUID:88111517; PMID:3501369
16	69	24.0	279	T05421	A:Accession: S03520
17	69	24.0	405	S65459	A:Molecule type: mRNA
18	69	24.0	151	T8535	A:Residues: 1-240 <ARU>
19	68.5	23.8	192	JCS876	A:Cross-references: EMBL:X06180; NID:g29819; PIDN:CAA29546.1; PID:g732757
20	68.5	23.8	347	2 G83171	C:Genetics:
21	68.5	23.8	684	T28603	A:Gene: GDB:CD7
22	68	23.6	801	2 T39108	A:Cross-references: GDB:119770; OMIM:186820
23	68	23.6	907	E86136	A:Map Position: 17q25.2-17q25.3
24	68	23.6	1173	T31421	A:Introns: 28/1
25	68	23.6	2240	T3057	C:Keywords: glycoprotein; membrane protein; surface antigen; tandem repeat
26	67.5	23.4	211	2 T55911	F1/25/Domain: signal sequence #status Predicted <SIG>
27	67.5	23.4	237	2 S46964	F1/25/Domain: signal sequence #status Predicted <MAT>
28	67.5	23.4	377	A44018	F145-180/Region: 9-residue repeats (X-P-X-A-S-I-L-P)
29	67	23.3	191	2 P84522	F145-180/Region: 9-residue repeats (X-P-X-A-S-I-L-P)

ALIGNMENTS

RESULT 1	Query Match	Length	DB ID	Description
A39016	98.6%	240	A39016	T-cell surface glycoprotein CD7 precursor - human
	Score 284; DB 2; Length 240;			
	Best Local Similarity 98.3%; Pred. No. 2.3e-19; Matches 57; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			
	Db 147 PRASALPAPPTGALPDQTVISPLGLGGLGVACVLARTR 58			
	1 PRASALPAPPTGALPDQTVISPLGLGGLGVACVLARTR 58			
	2 T30709 core protein homolog 107L - <i>Molluscum contagiosum</i> virus 1			
	N:Alternate name: MCL017L			
	C:Species: <i>Molluscum contagiosum</i> virus 1			
	C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004			
	C:Accession: T30709			
	R.Sentenac, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moeb, B.			
	Science 273, 813-816, 1996			

gene ox40 protein
myoblast determina
proline-rich prote
mucin 1 precursor,
rod shape-determin
probable dihydrodiol
related to cytoske
hypothetical prote
peptidyl-prolyl ci
factor VII intron
hypothetical prote
probable PBP prote
arabinogalactan-pr
18K14-10 (imported
hypothetical prote
probable membrane

A;Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host re
A;Reference number: 220876; MUID:96325459; PMID:8670425
A;Accession: T0709
A;Status: Preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residue: 1-421; <STO>
A;Cross-references: UNIPROT:Q98274; EMBL:U60315; PIDN:AC55235.1
C;Genetics:
A;Note: MC107L

RESULT 3

Query Match 27.8%; Score 80; DB 2; Length 421;
Best Local Similarity 54.5%; Pred. No. 2;4; Mismatches 15; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 3 ASALPAPPTGSLDPPDTASALDPDPPASALPA 35
Db 220 APACPAPATSPACPAPATAPACPAPATAPACPA 252

RESULT 4

oleosin-like protein - rape
C;Species: Brassica napus (rape)
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004
C;Accession: T0134
R;Hong, H.P.; Robb, J.H.; Gerster, J.L.; Rigas, S.; Datla, R.S.; Hatzopoulos, P.; Scopes
Plant Mol. Biol. 34, 549-555, 1997
A;Title: Promoter sequences from two different Brassica napus tapetal oleosin-like genes
A;Reference number: 216373; MUID:97369377; PMID:9225865
A;Accession: T0134
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-370 <HON>
A;Cross-references: UNIPROT:P93066; EMBL:Y08986; NID:91769971; PIDN:CAA70173.1; PID:9176
A;Experimental source: cv. Jet Neuf
C;Genetics:
A;Introns: 105/2; 184/2

Query Match 26.7%; Score 77; DB 2; Length 375;
Best Local Similarity 47.4%; Pred. No. 4;1; Mismatches 1; Indels 0; Gaps 0;
Matches 18; Conservative 1; Mismatches 19; Indels 0; Gaps 0;

Qy 1 PRASALLAPPTGSLDPPDTASALDPDPPASALPA 38
Db 213 PEAPAAPAAPAAPAAPAAPAAPAAPAPEAPA 250

RESULT 5

oleosin-like protein - rape
C;Species: Brassica napus (rape)
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004
C;Accession: T0134
R;Hong, H.P.; Robb, J.H.; Gerster, J.L.; Rigas, S.; Datla, R.S.; Hatzopoulos, P.; Scopes
Plant Mol. Biol. 34, 549-555, 1997
A;Title: Promoter sequences from two different Brassica napus tapetal oleosin-like genes
A;Reference number: 216373; MUID:97369377; PMID:9225865
A;Accession: T0134
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-559 <HON>
A;Cross-references: UNIPROT:Q8MNQ9; EMBL:AF00298; PIDN:AC48255.1; GSPDB:GN00022; CBSP:V
C;Genetics:
A;Experimental source: strain Bristol N2; clone W03D2
C;Accession: T28770
A;Map position: 4-13; 88/3; 115/3; 146/3; 173/3
A;Gene: CEPB:W03D2.1
A;Map position: 4-13; 88/3; 115/3; 146/3; 173/3
A;Introns: 40/3; 88/3; 115/3; 146/3; 173/3
C;Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl-terminal homology
Query Match 26.0%; Score 75; DB 2; Length 539;
Best Local Similarity 47.1%; Pred. No. 8;7; Mismatches 1; Indels 0; Gaps 0;
Matches 16; Conservative 2; Mismatches 14; Indels 2; Gaps 1;

Qy 1 PRASALLAPPTGSLDPPDTASALDPDPPASALPA 34
Db 288 PRTGSPPPPPIGS--PPPPPIAGGSPPPRAGSPP 319

RESULT 6

oleosin-like protein - rape
C;Species: Brassica napus (rape)
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004
C;Accession: T0134
R;Hong, H.P.; Robb, J.H.; Gerster, J.L.; Rigas, S.; Datla, R.S.; Hatzopoulos, P.; Scopes
Plant Mol. Biol. 34, 549-555, 1997
A;Title: Promoter sequences from two different Brassica napus tapetal oleosin-like genes
A;Reference number: 216373; MUID:97369377; PMID:9225865
A;Accession: T0134
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-559 <HON>
A;Cross-references: UNIPROT:Q8MNQ9; EMBL:AF00298; PIDN:AC48255.1; GSPDB:GN00022; CBSP:V
C;Genetics:
A;Gene: CEPB:W03D2.1
A;Map position: 4-13; 88/3; 115/3; 146/3; 173/3
A;Introns: 40/3; 88/3; 115/3; 146/3; 173/3
C;Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl-terminal homology
Query Match 26.0%; Score 75; DB 2; Length 891;
Best Local Similarity 42.9%; Pred. No. 14; Mismatches 11; Indels 6; Gaps 1;
Matches 15; Conservative 3; Mismatches 11; Indels 6; Gaps 1;

Qy 7 PAP-----PQSALDPPQTASALPPPPASALPA 35
Db 441 PSPVARLURDPTGARLPSIQRRLPSPPVQAQLPS 475

RESULT 7

oleosin-like protein - rape
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T28770
R;Rohlfing, T.; Wohldmann, P.
Submitted to the EMBL Data Library, June 1997
A;Description: The sequence of C. elegans coomid W03D2.
A;Reference number: 220519
A;Accession: T28770
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-559 <HON>
A;Cross-references: UNIPROT:Q8MNQ9; EMBL:AF00298; PIDN:AC48255.1; GSPDB:GN00022; CBSP:V
C;Genetics:
A;Experimental source: strain Bristol N2; clone W03D2
C;Accession: T28770
A;Map position: 4-13; 88/3; 115/3; 146/3; 173/3
A;Gene: CEPB:W03D2.1
A;Map position: 4-13; 88/3; 115/3; 146/3; 173/3
A;Introns: 40/3; 88/3; 115/3; 146/3; 173/3
C;Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl-terminal homology
Query Match 26.0%; Score 75; DB 2; Length 539;
Best Local Similarity 47.1%; Pred. No. 8;7; Mismatches 1; Indels 0; Gaps 0;
Matches 16; Conservative 2; Mismatches 14; Indels 2; Gaps 1;

Qy 1 PRASALLAPPTGSLDPPDTASALDPDPPASALPA 34
Db 288 PRTGSPPPPPIGS--PPPPPIAGGSPPPRAGSPP 319

RESULT 8

oleosin-like protein - rape
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: G84693
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alonso, C.;Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Deward, K.;Ansen, N.F.; Hughes, B.; Huizar, L.; Nature 408, 816-820, 2000
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: D95728
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alonso, C.;Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Deward, K.;Ansen, N.F.; Hughes, B.; Huizar, L.; Nature 408, 816-820, 2000
C;Accession: G84693
R;Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanken, S.E.; Umeyam, L.; Tallon, L.;euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Ventur, J.; C.;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;C.;Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marziali, C.;Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Authors: Salzberg, S.L.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Sun, H.; Tallon, A.;Author: Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.; M.; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:1617187
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-891 <STO>
A;Cross-references: UNIPROT:Q9ZWW8; GB:AE002093; NID:93980411; PIDN:AC95214.1; GSPDB:GN00022; CBSP:V
C;Genetics:
A;Gene: ATG9210
A;Map position: 2

RESULT 9

oleosin-like protein - rape
C;Species: Volvox carteri (fragment)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: F24013.3
A;Map position: 1

oleosin-like protein - rape
C;Species: Volvox carteri (fragment)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: F24013.3
A;Map position: 1

C;Species: *Volvox carteri*
 C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
 C;Accession: S22657; S21006
 R;Brtl, H.; Hallmann, A.; Wenzl, S.; Sumper, M.
 EMBO J. 11, 205-2062, 1992
 A;Title: A novel extensin that may organize extracellular matrix biogenesis in *Volvox carteri*
 A;Reference number: S22697; MUID:9289669; PMID:1600938
 A;Accession: T36045
 A;Molecule type: mRNA
 A;Residues: 1-464 <HAL>
 A;Cross-references: UNIPROT:Q41645; EMBL:X65165; NID:921991; PIDN:CAA46283.1; PID:g21992
 C;Keywords: glycoprotein

Query Match 25.7%; Score 74; DB 2; Length 464;
 Best Local Similarity 47.1%; Pred. No. 9.4;
 Matches 16; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
 Qy 1 PRASALPAPTPGSALPDQNTASALPDPPASALP 34
 Db 344 PRPSPSPPSPSSPSPPPVVSPPPPPRASPP 377

RESULT 8

microfilarial bleach protein - nematode (*Litomoboides carinini*)
 C;Species: *Litomoboides carinini*
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
 C;Accession: S41966
 R;Hirnmann, J.; Schnauffer, A.; Hintz, M.; Conraths, F.J.; Stirn, S.; Zahner, H.; Hobom, G.;Description: *Brugia spp.* and *Litomoboides carinini*: characterization of the shp2 gene
 A;Reference: T36045
 A;Accession: S41966
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-215 <HIR>
 A;Cross-references: UNIPROT:Q25256; EMBL:235443; NID:9516387; PID:9516388
 A;Genetics: C;Genetics:
 A;Introns: 19/3

Query Match 25.3%; Score 73; DB 2; Length 482;
 Best Local Similarity 44.4%; Pred. No. 12; Mismatches 4; Indels 2; Gaps 1;
 Matches 16; Conservative 0; Mismatches 14; Indels 2; Gaps 1;
 Qy 1 PRASALP--APPGSALEDPDQNTASALPDPPASALP 34
 Db 185 PTATPATPATAPPVAPPTRAVPPPPALASPP 220

RESULT 9

E66194 hypothetical protein [imported] - *Arabidopsis thaliana*
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
 C;Accession: E66194
 R;Theologis, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; aronen, N.F.; Hughes, B.; Ruiz, L.
 Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.; Cai, Li; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marzilli, A.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Asanen, N.F.; Hughes, B.; Ruiz, L.
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinm, P.; Southwick, A.M.; Sun, H.; Tallon, I.; Kert, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A;Reference number: A66141; MUID:21016719; PMID:11130712
 A;Accession: E66194
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-614 <STO>
 A;Cross-references: UNIPROT:Q91INFO; GB:AB005172; NID:98810458; PIDN:AAF80119.1; GSPDB:GN019
 C;Genetics: C;Genetics:
 A;Map Position: 1

Query Match 25.3%; Score 73; DB 2; Length 614;
 Best Local Similarity 43.4%; Pred. No. 15; Mismatches 21; Indels 4; Gaps 2;
 Matches 23; Conservative 5; Mismatches 21; Indels 4; Gaps 2;

Query Match 25.3%; Score 73; DB 2; Length 614;
 Best Local Similarity 43.4%; Pred. No. 15; Mismatches 21; Indels 4; Gaps 2;
 Matches 23; Conservative 5; Mismatches 21; Indels 4; Gaps 2;

Qy 3 ASALPAPTPGSALPDQNTASALPDPPASALP 54
 Db 94 ASALPSAPVSSSPEPEPSIAMLNDLNRLVIAAVACLGVTISFLA--GASCVL 143

RESULT 10

T36600 acetyl-CoA carboxylase (EC 6.4.1.2), biotin carboxyl carrier chain precursor - soybean
 N;Contains: biotin carboxyl carrier chain
 C;Species: Glycine max (soybean)
 C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
 C;Accession: T06600
 R;Nielsen, N.C.; Reverdatto, S.V.; Beilinson, V.A.
 Submitted to the EMBL Data Library, November 1995

Query Match 25.3%; Score 73; DB 2; Length 418;
 Best Local Similarity 32.1%; Pred. No. 11; Mismatches 11; Indels 27; Gaps 0;
 Matches 18; Conservative 11; Mismatches 27; Indels 0; Gaps 0;

Qy 3 ASALPAPTPGSALPDQNTASALPDPPASALP 54

Db 94 ASALPSAPVSSSPEPEPSIAMLNDLNRLVIAAVACLGVTISFLA--GASCVL 143

RESULT 11

G02953 beta-3-adrenergic receptor - rhesus macaque
 C;Species: *Macaca mulatta* (rhesus macaque)
 C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
 C;Accession: G02953
 R;Lowe, A.L.; Weston, J.; Shuldiner, A.R.
 submitted to the EMBL Data Library, July 1996
 A;Reference number: H01989
 A;Accession: G02953
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-418 <LOW>
 A;Cross-references: UNIPROT:Q28524; EMBL:U63592; NID:91458230; PIDN:AAB53939.1; PID:g145
 C;Genetics: C;Genetics:
 A;Introns: 402/1
 C;Superfamily: vertebrate rhodopsin

RESULT 12

T06600 acetyl-CoA carboxylase (EC 6.4.1.2), biotin carboxyl carrier chain precursor - soybean
 N;Contains: biotin carboxyl carrier chain
 C;Species: Glycine max (soybean)
 C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
 C;Accession: T06600
 R;Nielsen, N.C.; Reverdatto, S.V.; Beilinson, V.A.
 Submitted to the EMBL Data Library, November 1995

A;Reference number: 215788
 A;Accession: T06600
 A;Status: translated from GB/EMBL/DDJB
 A;Molecule type: mRNA
 A;Residues: 1-262 <NIE>
 A;Cross-references: UNIPROT:Q42783; EMBL:U40666; NID:9143318; PIDN:AAF67836.1; PID:9114
 A;Experimental source: strain Resnik
 A;Genetics:
 A;Gene: accB-1
 A;Genome: nuclear
 A;Function: <BCC>
 A;Description: biotin carboxyl carrier chain is responsible for binding of biotin
 A;Pathway: fatty acid biosynthesis
 C;Superfamily: biotin carboxyl carrier protein; lipoyl/biotin-binding homology
 C;Keywords: biotin metabolism; chloroplast; fatty acid biosynthesis; ligase
 F;1/47/Domain: transit peptide (chloroplast) #status predicted <TMP>
 F;48-262/Product: acetyl-CoA carboxylase, biotin carboxyl carrier chain #status predicted
 Query Match 24.7%; Score 71; DB 2; Length 262;
 Best Local Similarity 41.7%; Pred. No. 10; Matches 15; Conservative 5; Mismatches 16; Indels 0; Gaps 0;
 Db 146 PPPALPPPPVPASTPAPLARAKTPTPSAPVKA 181

RESULT 13
 C75286 hypothetical protein - Deinococcus radiodurans (strain R1)
 C;Species: Deinococcus radiodurans
 C;Accession: C75286 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 R;White, O.; Eisen, J.A.; Heidelberg, J.P.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 S.; Smith, H.O.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
 Science 286, 1571-1577, 1999
 A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A;Reference number: A75250; MUBD:20036896; PMID:10567266
 A;Accession: C75286
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-559 <WHI>
 A;Cross-references: UNIPROT:Q9RY4; GB:AE002065; GB:AE000513; NID:96460149; PIDN:AAF1189
 A;Experimental source: strain R1
 C;Genetics:
 A;Gene: DR2348
 A;Map position: 1
 C;Superfamily: Deinococcus radiodurans hypothetical protein DR2348
 Query Match 24.5%; Score 70.5; DB 2; Length 559;
 Best Local Similarity 35.7%; Pred. No. 23; Matches 20; Conservative 4; Mismatches 15; Indels 17; Gaps 2;
 Db 1 PRASALPAPPTGSAALPDQFASAIFD-----PPAS--ALPAIAV 39
 258 PATSGGAPASPDTTIDPDTATDGGTSDG3DLTFFGVTEQMPAAATEPAPAPA 313

RESULT 14
 Q8BE3 BHUFL1 protein - human herpesvirus 4 (strain B95-8)
 C;Species: human herpesvirus 4, Epstein-Barr virus
 C;Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 09-Jul-2004
 C;Accession: A03742
 R;Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.
 Mol. Biol. Med. 1, 2145, 1983

A;Title: Sequence analysis of the 17/166 bp EcoRI fragment C or B95-8 Epstein-Barr virus.
 A;Accession: A03442
 A;Residues: 1-660 <BAN>
 A;Cross-references: UNIPROT:P03181
 R;Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.L.; Farrell, P.J.; Gibson, T.J.; He
 Nature 310, 207-211, 1984
 A;Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.
 A;Reference number: A03794; PMID:84207617; PMID:6087149
 A;Comments: annotation; protein coding region
 C;Comment: The sequence contains four perfect repeats (residues 149-273, 274-398, 399-52:
 C;Superfamily: human herpesvirus 4 BHlf1 protein

 Query Match 24.5%; Score 70.5; DB 1; Length 660;
 Best Local Similarity 41.0%; Pred. No. 27;
 Matches 16; Conservative 4; Mismatches 14; Indels 5; Gaps 1;
 Qy 1 PRASALPAPPTGSAIPD-----POTASALPDPPAASALP 34
 Db 192 PGTPAPGPGGAAVPSPGATPHPERGGSPADPPAARLP 230

 RESULT 15
 T14150 vesicle associated protein 1 - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C;Accession: T14150
 R;Shugrue, C.A.; Peters, H.; Matovcik, L.M.; Kolen, E.R.; Czernik, A.J.; Hubbard, A.; Gor
 submitted to the EMBL Data Library, November 1997
 A;Reference number: ZI7887
 A;Accession: T14150
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: mRNA
 A;Residues: 1-1249 <SHU>
 A;Cross-references: UNIPROT:Q9ZQ1; EMBL:AF034582; NID:94104320; PID:94104321; PNID:AAD01
 A;Experimental source: liver
 A;Genetics:
 C;Gene: VAP1

 Query Match 24.1%; Score 69.5; DB 2; Length 1249;
 Best Local Similarity 37.3%; Pred. No. 61; Gaps 2;
 Matches 19; Conservative 4; Mismatches 13; Indels 15; Gaps 2;
 Qy 1 PRASALPAPPT-----GSAIPDPTOTASALP-----DPPAASALPAA 36
 Db 965 PTSSSSAPLPPPPSSGGASFOHGGPGAPPSSAYALPPGTGTGTPPASELPAS 1015

 Search completed: March 7, 2005, 07:21:01
 Job time : 6.8765 secs